

SEQUENCE LISTING

SEQ. ID No. 1

LENGTH: 271

TYPE: amino acid

5 STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

10 Ala Ile Pro Ala Pro Thr Asp Leu Lys Phe Thr Gln Val Thr Pro  
1 5 10 15  
Thr Ser Leu Ser Ala Gln Trp Thr Pro Pro Asn Val Gln Leu Thr  
20 25 30  
Gly Tyr Arg Val Arg Val Thr Pro Lys Glu Lys Thr Gly Pro Met  
35 40 45  
15 Lys Glu Ile Asn Leu Ala Pro Asp Ser Ser Ser Val Val Val Ser  
50 55 60  
Gly Leu Met Val Ala Thr Lys Tyr Glu Val Ser Val Tyr Ala Leu  
65 70 75  
Lys Asp Thr Leu Thr Ser Arg Pro Ala Gln Gly Val Val Thr Thr  
20 80 85 90  
Leu Glu Asn Val Ser Pro Pro Arg Arg Ala Arg Val Thr Asp Ala  
95 100 105  
Thr Glu Thr Thr Ile Thr Ile Ser Trp Arg Thr Lys Thr Glu Thr  
110 115 120

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Ile	Thr	Gly	Phe	Gln	Val	Asp	Ala	Val	Pro	Ala	Asn	Gly	Gln	Thr
				125					130					135
Pro	Ile	Gln	Arg	Thr	Ile	Lys	Pro	Asp	Val	Arg	Ser	Tyr	Thr	Ile
				140					145					150
Thr	Gly	Leu	Gln	Pro	Gly	Thr	Asp	Tyr	Lys	Ile	Tyr	Leu	Tyr	Thr
				155					160					165
Leu	Asn	Asp	Asn	Ala	Arg	Ser	Ser	Pro	Val	Val	Ile	Asp	Ala	Ser
				170					175					180
Thr	Ala	Ile	Asp	Ala	Pro	Ser	Asn	Leu	Arg	Phe	Leu	Ala	Thr	Thr
				185					190					195
Pro	Asn	Ser	Leu	Leu	Val	Ser	Trp	Gln	Pro	Pro	Arg	Ala	Arg	Ile
				200					205					210
Thr	Gly	Tyr	Ile	Ile	Lys	Tyr	Glu	Lys	Pro	Gly	Ser	Pro	Pro	Arg
				215					220					225
Glu	Val	Val	Pro	Arg	Pro	Arg	Pro	Gly	Val	Thr	Glu	Ala	Thr	Ile
				230					235					240
Thr	Gly	Leu	Glu	Pro	Gly	Thr	Glu	Tyr	Thr	Ile	Tyr	Val	Ile	Ala
				245					250					255
Leu	Lys	Asn	Asn	Gln	Lys	Ser	Glu	Pro	Leu	Ile	Gly	Arg	Lys	Lys
				260					265					270
Thr														

SEQ. ID No. 2

LENGTH: 25

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

5 Asp Glu Leu Pro Gln Leu Val Thr Leu Pro His Pro Asn Leu His  
1 5 10 15  
Gly Pro Glu Ile Leu Asp Val Pro Ser Thr  
20 25

SEQ. ID No. 3

10 LENGTH: 155

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

15 SEQUENCE:

20 Met Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala Leu Pro Glu Asp  
1 5 10 15  
Gly Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro Lys  
20 25 30  
Arg Leu Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro  
35 40 45  
Asp Gly Arg Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile  
50 55 60  
Lys Leu Gln Leu Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys

65 70 75  
Gly Val Cys Ala Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg  
80 85 90  
Leu Leu Ala Ser Lys Cys Val Thr Asp Glu Cys Phe Phe Phe Glu  
5 95 100 105  
Arg Leu Glu Ser Asn Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr  
110 115 120  
Thr Ser Trp Tyr Val Ala Leu Lys Arg Thr Gly Gln Tyr Lys Leu  
125 130 135  
10 Gly Ser Lys Thr Gly Pro Gly Gln Lys Ala Ile Leu Phe Leu Pro  
140 145 150  
Met Ser Ala Lys Ser  
155

SEQ. ID No. 4

15 LENGTH: 432

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

20 SEQUENCE:

Pro Thr Asp Leu Arg Phe Thr Asn Ile Gly Pro Asp Thr Met Arg  
1 5 10 15  
Val Thr Trp Ala Pro Pro Pro Ser Ile Asp Leu Thr Asn Phe Leu  
20 25 30

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215	220	225
Thr Val Pro Gly Ser Lys Ser Thr Ala	Thr Ile Ser Gly Leu Lys	
230	235	240
Pro Gly Val Asp Tyr Thr Ile Thr Val	Tyr Ala Val Thr Gly Arg	
245	250	255
Gly Asp Ser Pro Ala Ser Ser Lys Pro	Ile Ser Ile Asn Tyr Arg	
260	265	270
Thr Glu Ile Asp Lys Pro (Ser) Met Ala	Ala Gly Ser Ile Thr Thr	
275	280	285
Leu Pro Ala Leu Pro Glu Asp Gly Gly	Ser Gly Ala Phe Pro Pro	
290	295	300
Gly His Phe Lys Asp Pro Lys Arg Leu	Tyr Cys Lys Asn Gly Gly	
305	310	315
Phe Phe Leu Arg Ile His Pro Asp Gly	Arg Val Asp Gly Val Arg	
320	325	330
Glu Lys Ser Asp Pro His Ile Lys Leu	Gln Leu Gln Ala Glu Glu	
335	340	345
Arg Gly Val Val Ser Ile Lys Gly Val	Cys Ala Asn Arg Tyr Leu	
350	355	360
Ala Met Lys Glu Asp Gly Arg Leu Leu	Ala Ser Lys Cys Val Thr	
365	370	375
Asp Glu Cys Phe Phe Phe Glu Arg Leu	Glu Ser Asn Asn Tyr Asn	
380	385	390
Thr Tyr Arg Ser Arg Lys Tyr Thr Ser	Trp Tyr Val Ala Leu Lys	
395	400	405

Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly Gln  
410 415 420  
Lys Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser  
425 430

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SEQ. ID No. 5

LENGTH: 457

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

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MOLECULAR TYPE: peptide

SEQUENCE:

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Pro Thr Asp Leu Arg Phe Thr Asn Ile Gly Pro Asp Thr Met Arg  
1 5 10 15  
Val Thr Trp Ala Pro Pro Pro Ser Ile Asp Leu Thr Asn Phe Leu  
20 25 30  
Val Arg Tyr Ser Pro Val Lys Asn Glu Glu Asp Val Ala Glu Leu  
35 40 45  
Ser Ile Ser Pro Ser Asp Asn Ala Val Val Leu Thr Asn Leu Leu  
50 55 60  
20 Pro Gly Thr Glu Tyr Val Val Ser Val Ser Ser Val Tyr Glu Gln  
65 70 75  
His Glu Ser Thr Pro Leu Arg Gly Arg Gln Lys Thr Gly Leu Asp  
80 85 90  
Ser Pro Thr Gly Ile Asp Phe Ser Asp Ile Thr Ala Asn Ser Phe

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	95	100	105
Thr Val His Trp	Ile Ala Pro Arg Ala	Thr Ile Thr Gly Tyr	Arg
	110	115	120
Ile Arg His His	Pro Glu His Phe Ser	Gly Arg Pro Arg	Glu Asp
	125	130	135
Arg Val Pro His	Ser Arg Asn Ser Ile	Thr Leu Thr Asn	Leu Thr
	140	145	150
Pro Gly Thr Glu	Tyr Val Val Ser Ile	Val Ala Leu Asn	Gly Arg
	155	160	165
Glu Glu Ser Pro	Leu Leu Ile Gly Gln	Gln Ser Thr Val	Ser Asp
	170	175	180
Val Pro Arg Asp	Leu Glu Val Val Ala	Ala Thr Pro Thr	Ser Leu
	185	190	195
Leu Ile Ser Trp	Asp Ala Pro Ala Val	Thr Val Arg Tyr	Tyr Arg
	200	205	210
Ile Thr Tyr Gly	Glu Thr Gly Gly Asn	Ser Pro Val Gln	Glu Phe
	215	220	225
Thr Val Pro Gly	Ser Lys Ser Thr Ala	Thr Ile Ser Gly	Leu Lys
	230	235	240
Pro Gly Val Asp	Tyr Thr Ile Thr Val	Tyr Ala Val Thr	Gly Arg
	245	250	255
Gly Asp Ser Pro	Ala Ser Ser Lys Pro	Ile Ser Ile Asn	Tyr Arg
	260	265	270
Thr Glu Ile Asp	Lys Pro Ser Met Ala	Ala Gly Ser Ile	Thr Thr
	275	280	285





SEQ. ID No. 6

LENGTH: 186

TYPE: amino acid

STRANDEDNESS: single

5 TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

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Gly	Ile	Arg	Gly	Leu	Lys	Gly	Thr	Lys	Gly	Glu	Lys	Gly	Glu	Asp
1				5				10					15	
Gly	Phe	Pro	Gly	Phe	Lys	Gly	Asp	Met	Gly	Ile	Lys	Gly	Asp	Arg
				20				25					30	
Gly	Glu	Ile	Gly	Pro	Pro	Gly	Pro	Arg	Gly	Glu	Asp	Gly	Pro	Glu
				35				40					45	
Gly	Pro	Lys	Gly	Arg	Gly	Gly	Pro	Asn	Gly	Asp	Pro	Gly	Pro	Leu
				50				55					60	
Gly	Pro	Pro	Gly	Glu	Lys	Gly	Lys	Leu	Gly	Val	Pro	Gly	Leu	Pro
				65				70					75	
Gly	Tyr	Pro	Gly	Arg	Gln	Gly	Pro	Lys	Gly	Ser	Ile	Gly	Phe	Pro
				80				85					90	
Gly	Phe	Pro	Gly	Ala	Asn	Gly	Glu	Lys	Gly	Gly	Arg	Gly	Thr	Pro
				95				100					105	
Gly	Lys	Pro	Gly	Pro	Arg	Gly	Gln	Arg	Gly	Pro	Thr	Gly	Pro	Arg
				110				115					120	
Gly	Glu	Arg	Gly	Pro	Arg	Gly	Ile	Thr	Gly	Lys	Pro	Gly	Pro	Lys
				125				130					135	

Gly Asn Ser Gly Gly Asp Gly Pro Ala Gly Pro Pro Gly Glu Arg  
140 145 150  
Gly Pro Asn Gly Pro Gln Gly Pro Thr Gly Phe Pro Gly Pro Lys  
155 160 165  
5 Gly Pro Pro Gly Pro Pro Gly Lys Asp Gly Leu Pro Gly His Pro  
170 175 180  
Gly Gln Arg Gly Glu Thr  
185

SEQ. ID No. 7

LENGTH: 464

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

Pro Thr Asp Leu Arg Phe Thr Asn Ile Gly Pro Asp Thr Met Arg  
1 5 10 15  
Val Thr Trp Ala Pro Pro Pro Ser Ile Asp Leu Thr Asn Phe Leu  
20 25 30  
20 Val Arg Tyr Ser Pro Val Lys Asn Glu Glu Asp Val Ala Glu Leu  
35 40 45  
Ser Ile Ser Pro Ser Asp Asn Ala Val Val Leu Thr Asn Leu Leu  
50 55 60  
Pro Gly Thr Glu Tyr Val Val Ser Val Ser Ser Val Tyr Glu Gln

		65		70		75
	His Glu Ser Thr Pro Leu Arg Gly Arg Gln Lys Thr Gly Leu Asp					
		80		85		90
	Ser Pro Thr Gly Ile Asp Phe Ser Asp Ile Thr Ala Asn Ser Phe					
5		95		100		105
	Thr Val His Trp Ile Ala Pro Arg Ala Thr Ile Thr Gly Tyr Arg					
		110		115		120
	Ile Arg His His Pro Glu His Phe Ser Gly Arg Pro Arg Glu Asp					
		125		130		135
10	Arg Val Pro His Ser Arg Asn Ser Ile Thr Leu Thr Asn Leu Thr					
		140		145		150
	Pro Gly Thr Glu Tyr Val Val Ser Ile Val Ala Leu Asn Gly Arg					
		155		160		165
	Glu Glu Ser Pro Leu Leu Ile Gly Gln Gln Ser Thr Val Ser Asp					
15		170		175		180
	Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu					
		185		190		195
	Leu Ile Ser Trp Asp Ala Pro Ala Val Thr Val Arg Tyr Tyr Arg					
		200		205		210
20	Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe					
		215		220		225
	Thr Val Pro Gly Ser Lys Ser Thr Ala Thr Ile Ser Gly Leu Lys					
		230		235		240
	Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Gly Arg					
25		245		250		255

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Gly	Asp	Ser	Pro	Ala	Ser	Ser	Lys	Pro	Ile	Ser	Ile	Asn	Tyr	Arg
				260					265					270
Thr	Glu	Ile	Asp	Lys	Pro	Ser	Met	Gly	Ile	Arg	Gly	Leu	Lys	Gly
				275					280					285
Thr	Lys	Gly	Glu	Lys	Gly	Glu	Asp	Gly	Phe	Pro	Gly	Phe	Lys	Gly
				290					295					300
Asp	Met	Gly	Ile	Lys	Gly	Asp	Arg	Gly	Glu	Ile	Gly	Pro	Pro	Gly
				305					310					315
Pro	Arg	Gly	Glu	Asp	Gly	Pro	Glu	Gly	Pro	Lys	Gly	Arg	Gly	Gly
				320					325					330
Pro	Asn	Gly	Asp	Pro	Gly	Pro	Leu	Gly	Pro	Pro	Gly	Glu	Lys	Gly
				335					340					345
Lys	Leu	Gly	Val	Pro	Gly	Leu	Pro	Gly	Tyr	Pro	Gly	Arg	Gln	Gly
				350					355					360
Pro	Lys	Gly	Ser	Ile	Gly	Phe	Pro	Gly	Phe	Pro	Gly	Ala	Asn	Gly
				365					370					375
Glu	Lys	Gly	Gly	Arg	Gly	Thr	Pro	Gly	Lys	Pro	Gly	Pro	Arg	Gly
				380					385					390
Gln	Arg	Gly	Pro	Thr	Gly	Pro	Arg	Gly	Glu	Arg	Gly	Pro	Arg	Gly
				395					400					405
Ile	Thr	Gly	Lys	Pro	Gly	Pro	Lys	Gly	Asn	Ser	Gly	Gly	Asp	Gly
				410					415					420
Pro	Ala	Gly	Pro	Pro	Gly	Glu	Arg	Gly	Pro	Asn	Gly	Pro	Gln	Gly
				425					430					435
Pro	Thr	Gly	Phe	Pro	Gly	Pro	Lys	Gly	Pro	Pro	Gly	Pro	Pro	Gly

440 445 450  
Lys Asp Gly Leu Pro Gly His Pro Gly Gln Arg Gly Glu Thr  
455 460

SEQ. ID No. 8

5 LENGTH: 489

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

Pro Thr Asp Leu Arg Phe Thr Asn Ile Gly Pro Asp Thr Met Arg  
1 5 10 15  
Val Thr Trp Ala Pro Pro Pro Ser Ile Asp Leu Thr Asn Phe Leu  
20 25 30  
Val Arg Tyr Ser Pro Val Lys Asn Glu Glu Asp Val Ala Glu Leu  
35 40 45  
Ser Ile Ser Pro Ser Asp Asn Ala Val Val Leu Thr Asn Leu Leu  
50 55 60  
Pro Gly Thr Glu Tyr Val Val Ser Val Ser Ser Val Tyr Glu Gln  
20 65 70 75  
His Glu Ser Thr Pro Leu Arg Gly Arg Gln Lys Thr Gly Leu Asp  
80 85 90  
Ser Pro Thr Gly Ile Asp Phe Ser Asp Ile Thr Ala Asn Ser Phe  
95 100 105

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	290	295	300
Asp Met Gly Ile Lys Gly Asp Arg Gly Glu Ile Gly Pro Pro Gly			
	305	310	315
Pro Arg Gly Glu Asp Gly Pro Glu Gly Pro Lys Gly Arg Gly Gly			
	320	325	330
Pro Asn Gly Asp Pro Gly Pro Leu Gly Pro Pro Gly Glu Lys Gly			
	335	340	345
Lys Leu Gly Val Pro Gly Leu Pro Gly Tyr Pro Gly Arg Gln Gly			
	350	355	360
Pro Lys Gly Ser Ile Gly Phe Pro Gly Phe Pro Gly Ala Asn Gly			
	365	370	375
Glu Lys Gly Gly Arg Gly Thr Pro Gly Lys Pro Gly Pro Arg Gly			
	380	385	390
Gln Arg Gly Pro Thr Gly Pro Arg Gly Glu Arg Gly Pro Arg Gly			
	395	400	405
Ile Thr Gly Lys Pro Gly Pro Lys Gly Asn Ser Gly Gly Asp Gly			
	410	415	420
Pro Ala Gly Pro Pro Gly Glu Arg Gly Pro Asn Gly Pro Gln Gly			
	425	430	435
Pro Thr Gly Phe Pro Gly Pro Lys Gly Pro Pro Gly Pro Pro Gly			
	440	445	450
Lys Asp Gly Leu Pro Gly His Pro Gly Gln Arg Gly Ala Ser Asp			
	455	460	465
Glu Leu Pro Gln Leu Val Thr Leu Pro His Pro Asn Leu His Gly			
	470	475	480



Pro Glu Ile Leu Asp Val Pro Ser Thr

485

SEQ. ID No. 9

LENGTH: 36

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

AAACCATGGC AGTCAGCGAC GAGCTTCCCC AACTGG

36

SEQ. ID No. 10

LENGTH: 20

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

AATTGACAAA CCATCCATGG

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SEQ. ID No. 11

LENGTH: 33

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

CCATTAAAT CAGCTAGCAG CAGACATTGG AAG

33

SEQ. ID No. 12

LENGTH: 36

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

TCTAGAGGAT CCTTAGCTAG CGCCTCTCTG TCCAGG

36

SEQ. ID No. 13

LENGTH: 547

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

Ala Ala Ser Ala Ile Pro Ala Pro Thr Asp Leu Lys Phe Thr Gln

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Val Thr Pro Thr Ser Leu Ser Ala Gln Trp Thr Pro Pro Asn Val

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Gln	Leu	Thr	Gly	Tyr	Arg	Val	Arg	Val	Thr	Pro	Lys	Glu	Lys	Thr	
				35					40						45
Gly	Pro	Met	Lys	Glu	Ile	Asn	Leu	Ala	Pro	Asp	Ser	Ser	Ser	Val	
				50					55						60
Val	Val	Ser	Gly	Leu	Met	Val	Ala	Thr	Lys	Tyr	Glu	Val	Ser	Val	
				65					70						75
Tyr	Ala	Leu	Lys	Asp	Thr	Leu	Thr	Ser	Arg	Pro	Ala	Gln	Gly	Val	
				80					85						90
Val	Thr	Thr	Leu	Glu	Asn	Val	Ser	Pro	Pro	Arg	Arg	Ala	Arg	Val	
				95					100						105
Thr	Asp	Ala	Thr	Glu	Thr	Thr	Ile	Thr	Ile	Ser	Trp	Arg	Thr	Lys	
				110					115						120
Thr	Glu	Thr	Ile	Thr	Gly	Phe	Gln	Val	Asp	Ala	Val	Pro	Ala	Asn	
				125					130						135
Gly	Gln	Thr	Pro	Ile	Gln	Arg	Thr	Ile	Lys	Pro	Asp	Val	Arg	Ser	
				140					145						150
Tyr	Thr	Ile	Thr	Gly	Leu	Gln	Pro	Gly	Thr	Asp	Tyr	Lys	Ile	Tyr	
				155					160						165
Leu	Tyr	Thr	Leu	Asn	Asp	Asn	Ala	Arg	Ser	Ser	Pro	Val	Val	Ile	
				170					175						180
Asp	Ala	Ser	Thr	Ala	Ile	Asp	Ala	Pro	Ser	Asn	Leu	Arg	Phe	Leu	
				185					190						195
Ala	Thr	Thr	Pro	Asn	Ser	Leu	Leu	Val	Ser	Trp	Gln	Pro	Pro	Arg	
				200					205						210
Ala	Arg	Ile	Thr	Gly	Tyr	Ile	Ile	Lys	Tyr	Glu	Lys	Pro	Gly	Ser	

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Ala Asn Gly Gln Thr Pro Ile Gln Arg Thr Ile Lys Pro Asp Val		
	410	415 420
Arg Ser Tyr Thr Ile Thr Gly Leu Gln Pro Gly Thr Asp Tyr Lys		
	425	430 435
5 Ile Tyr Leu Tyr Thr Leu Asn Asp Asn Ala Arg Ser Ser Pro Val		
	440	445 450
Val Ile Asp Ala Ser Thr Ala Ile Asp Ala Pro Ser Asn Leu Arg		
	455	460 465
Phe Leu Ala Thr Thr Pro Asn Ser Leu Leu Val Ser Trp Gln Pro		
	470	475 480
Pro Arg Ala Arg Ile Thr Gly Tyr Ile Ile Lys Tyr Glu Lys Pro		
	485	490 495
Gly Ser Pro Pro Arg Glu Val Val Pro Arg Pro Arg Pro Gly Val		
	500	505 510
Thr Glu Ala Thr Ile Thr Gly Leu Glu Pro Gly Thr Glu Tyr Thr		
	515	520 525
Ile Tyr Val Ile Ala Leu Lys Asn Asn Gln Lys Ser Glu Pro Leu		
	530	535 540
Ile Gly Arg Lys Lys Thr Ser		
	545	

SEQ. ID No. 14

LENGTH: 826

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

Ala	Ala	Ser	Pro	Thr	Asp	Leu	Arg	Phe	Thr	Asn	Ile	Gly	Pro	Asp
				5					10					15
Thr	Met	Arg	Val	Thr	Trp	Ala	Pro	Pro	Pro	Ser	Ile	Asp	Leu	Thr
				20					25					30
Asn	Phe	Leu	Val	Arg	Tyr	Ser	Pro	Val	Lys	Asn	Glu	Glu	Asp	Val
				35					40					45
Ala	Glu	Leu	Ser	Ile	Ser	Pro	Ser	Asp	Asn	Ala	Val	Val	Leu	Thr
				50					55					60
Asn	Leu	Leu	Pro	Gly	Thr	Glu	Tyr	Val	Val	Ser	Val	Ser	Ser	Val
				65					70					75
Tyr	Glu	Gln	His	Glu	Ser	Thr	Pro	Leu	Arg	Gly	Arg	Gln	Lys	Thr
				80					85					90
Gly	Leu	Asp	Ser	Pro	Thr	Gly	Ile	Asp	Phe	Ser	Asp	Ile	Thr	Ala
				95					100					105
Asn	Ser	Phe	Thr	Val	His	Trp	Ile	Ala	Pro	Arg	Ala	Thr	Ile	Thr
				110					115					120
Gly	Tyr	Arg	Ile	Arg	His	His	Pro	Glu	His	Phe	Ser	Gly	Arg	Pro
				125					130					135
Arg	Glu	Asp	Arg	Val	Pro	His	Ser	Arg	Asn	Ser	Ile	Thr	Leu	Thr
				140					145					150
Asn	Leu	Thr	Pro	Gly	Thr	Glu	Tyr	Val	Val	Ser	Ile	Val	Ala	Leu
				155					160					165

Asn Gly Arg Glu Glu Ser Pro Leu Leu Ile Gly Gln Gln Ser Thr  
170 175 180  
Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro  
185 190 195  
5 Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Val Thr Val Arg  
200 205 210  
Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val  
215 220 225  
Gln Glu Phe Thr Val Pro Gly Ser Lys Ser Thr Ala Thr Ile Ser  
230 235 240  
Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val  
245 250 255  
Thr Gly Arg Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile Ser Ile  
260 265 270  
15 Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Thr Ser Ala Ile Pro  
275 280 285  
Ala Pro Thr Asp Leu Lys Phe Thr Gln Val Thr Pro Thr Ser Leu  
290 295 300  
Ser Ala Gln Trp Thr Pro Pro Asn Val Gln Leu Thr Gly Tyr Arg  
20 305 310 315  
Val Arg Val Thr Pro Lys Glu Lys Thr Gly Pro Met Lys Glu Ile  
320 325 330  
Asn Leu Ala Pro Asp Ser Ser Ser Val Val Val Ser Gly Leu Met  
335 340 345  
25 Val Ala Thr Lys Tyr Glu Val Ser Val Tyr Ala Leu Lys Asp Thr

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Asn	Gln	Lys	Ser	Glu	Pro	Leu	Ile	Gly	Arg	Lys	Lys	Thr	Ser	Ala
				545					550					555
Ile	Pro	Ala	Pro	Thr	Asp	Leu	Lys	Phe	Thr	Gln	Val	Thr	Pro	Thr
				560					565					570
Ser	Leu	Ser	Ala	Gln	Trp	Thr	Pro	Pro	Asn	Val	Gln	Leu	Thr	Gly
				575					580					585
Tyr	Arg	Val	Arg	Val	Thr	Pro	Lys	Glu	Lys	Thr	Gly	Pro	Met	Lys
				590					595					600
Glu	Ile	Asn	Leu	Ala	Pro	Asp	Ser	Ser	Ser	Val	Val	Val	Ser	Gly
				605					610					615
Leu	Met	Val	Ala	Thr	Lys	Tyr	Glu	Val	Ser	Val	Tyr	Ala	Leu	Lys
				620					625					630
Asp	Thr	Leu	Thr	Ser	Arg	Pro	Ala	Gln	Gly	Val	Val	Thr	Thr	Leu
				635					640					645
Glu	Asn	Val	Ser	Pro	Pro	Arg	Arg	Ala	Arg	Val	Thr	Asp	Ala	Thr
				650					655					660
Glu	Thr	Thr	Ile	Thr	Ile	Ser	Trp	Arg	Thr	Lys	Thr	Glu	Thr	Ile
				665					670					675
Thr	Gly	Phe	Gln	Val	Asp	Ala	Val	Pro	Ala	Asn	Gly	Gln	Thr	Pro
				680					685					690
Ile	Gln	Arg	Thr	Ile	Lys	Pro	Asp	Val	Arg	Ser	Tyr	Thr	Ile	Thr
				695					700					705
Gly	Leu	Gln	Pro	Gly	Thr	Asp	Tyr	Lys	Ile	Tyr	Leu	Tyr	Thr	Leu
				710					715					720
Asn	Asp	Asn	Ala	Arg	Ser	Ser	Pro	Val	Val	Ile	Asp	Ala	Ser	Thr

	725	730	735
	Ala Ile Asp Ala Pro Ser Asn Leu Arg Phe Leu Ala Thr Thr Pro		
	740	745	750
	Asn Ser Leu Leu Val Ser Trp Gln Pro Pro Arg Ala Arg Ile Thr		
5	755	760	765
	Gly Tyr Ile Ile Lys Tyr Glu Lys Pro Gly Ser Pro Pro Arg Glu		
	770	775	780
	Val Val Pro Arg Pro Arg Pro Gly Val Thr Glu Ala Thr Ile Thr		
	785	790	795
	Gly Leu Glu Pro Gly Thr Glu Tyr Thr Ile Tyr Val Ile Ala Leu		
	800	805	810
	Lys Asn Asn Gln Lys Ser Glu Pro Leu Ile Gly Arg Lys Lys Thr		
	815	820	825
	Ser		

SEQ. ID No. 15

LENGTH: 38

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

AAACCATGGC AGCTAGCGCT ATTCCTGCAC CAACTGAC

38

SEQ. ID No. 16

LENGTH: 36

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

5 MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

AAAGGATCCC TAACTAGTCT TTTTCCTTCC AATCAG

36

SEQ. ID No. 17

LENGTH: 1644

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (DNA encoding an  
artificial polypeptide)

SEQUENCE:

10  
15  
20  
ATGGCAGCTA GCGCTATTCC TGCACCAACT GACCTGAAGT TCACTCAGGT CACACCCACA 60  
AGCCTGAGCG CCCAGTGGAC ACCACCCAAT GTTCAGCTCA CTGGATATCG AGTGCGGGTG 120  
ACCCCCAAGG AGAAGACCGG ACCAATGAAA GAAATCAACC TTGCTCCTGA CAGCTCATCC 180  
GTGGTTGTAT CAGGACTTAT GGTGGCCACC AAATATGAAG TGAGTGTCTA TGCTCTTAAG 240  
GACACTTTGA CAAGCAGACC AGCTCAGGGT GTTGTACCA CTCTGGAGAA TGTCAGCCCA 300  
CCAAGAAGGG CTCGTGTGAC AGATGCTACT GAGACCACCA TCACCATTAG CTGGAGAACC 360  
AAGACTGAGA CGATCACTGG CTTCCAAGTT GATGCCGTTT CAGCCAATGG CCAGACTCCA 420  
ATCCAGAGAA CCATCAAGCC AGATGTCAGA AGCTACACCA TCACAGGTTT ACAACCAGGC 480  
ACTGACTACA AGATCTACCT GTACACCTTG AATGACAATG CTCGGAGCTC CCCTGTGGTC 540

ATCGACGCCT CCACTGCCAT TGATGCACCA TCCAACCTGC GTTTCCTGGC CACCACACCC 600  
AATTCCTTGC TGGTATCATG GCAGCCGCCA CGTGCCAGGA TTACCGGCTA CATCATCAAG 660  
TATGAGAAGC CTGGGTCTCC TCCCAGAGAA GTGGTCCCTC GGCCCCGCCC TGGTGTCACA 720  
GAGGCTACTA TTA CTGGCCT GGAACCGGGA ACCGAATATA CAATTTATGT CATTGCCCTG 780  
5 AAGAATAATC AGAAGAGCGA GCCCCTGATT GGAAGGAAAA AGACTAGCGC TATTCCTGCA 840  
CCA ACTGACC TGAAGTTCAC TCAGGTCACA CCCACAAGCC TGAGCGCCCA GTGGACACCA 900  
CCCAATGTTT AGCTCACTGG ATATCGAGTG CGGGTGACCC CCAAGGAGAA GACCGGACCA 960  
ATGAAAGAAA TCAACCTTGC TCCTGACAGC TCATCCGTGG TTGTATCAGG ACTTATGGTG 1020  
GCCACCAAAT ATGAAGTGAG TGTCTATGCT CTTAAGGACA CTTTGACAAG CAGACCAGCT 1080  
CAGGGTGTTG TCACCACTCT GGAGAATGTC AGCCCACCAA GAAGGGCTCG TGTGACAGAT 1140  
GCTACTGAGA CCACCATCAC CATTAGCTGG AGAACCAAGA CTGAGACGAT CACTGGCTTC 1200  
CAAGTTGATG CCGTTCCAGC CAATGGCCAG ACTCCAATCC AGAGAACCAT CAAGCCAGAT 1260  
GTCAGAAGCT ACACCATCAC AGGTTTACAA CCAGGCACTG ACTACAAGAT CTACCTGTAC 1320  
ACCTTGAATG ACAATGCTCG GAGCTCCCCT GTGGTCATCG ACGCCTCCAC TGCCATTGAT 1380  
GCACCATCCA ACCTGCGTTT CCTGGCCACC ACACCCAATT CCTTGCTGGT ATCATGGCAG 1440  
CCGCCACGTG CCAGGATTAC CGGCTACATC ATCAAGTATG AGAAGCCTGG GTCTCCTCCC 1500  
AGAGAAGTGG TCCCTCGGCC CCGCCCTGGT GTCACAGAGG CTACTATTAC TGGCCTGGAA 1560  
CCGGGAACCG AATATACAAT TTATGTCATT GCCCTGAAGA ATAATCAGAA GAGCGAGCCC 1620  
CTGATTGGAA GAAAAAAGAC TAGT 1644

20 SEQ. ID No. 18  
LENGTH: 37  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
25 MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

AAACCATGGC AGCTAGCCCC ACTGACCTGC GATTCAC

37

SEQ. ID No. 19

LENGTH: 38

5 TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

AAAAGATCTC TAACTAGTGG ATGGTTTGTC AATTTCTG

38

SEQ. ID No. 20

LENGTH: 2481

TYPE: nucleic acid

STRANDEDNESS: double

15 TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (DNA encoding an artificial polypeptide)

SEQUENCE:

ATGGCAGCTA GCCCCACTGA CCTGCGATTC ACCAACATTG GTCCAGACAC CATGCGTGTC 60

20 ACCTGGGCTC CACCCCCATC CATTGATTTA ACCAACTTCC TGGTGCGTTA CTCACCTGTG 120

AAAAATGAGG AAGATGTTGC AGAGTTGTCA ATTTCTCCTT CAGACAATGC AGTGGTCTTA 180

ACAAATCTCC TGCCTGGTAC AGAATATGTA GTGAGTGTCT CCAGTGTCTA CGAACAACAT 240

GAGAGCACAC CTCTTAGAGG AAGACAGAAA ACAGGTCTTG ATTCCCCAAC TGGCATTGAC 300

TTTTCTGATA TTACTGCCAA CTCTTTTACT GTGCACTGGA TTGCTCCTCG AGCCACCATC 360  
ACTGGCTACA GGATCCGCCA TCATCCCGAG CACTTCAGTG GGAGACCTCG AGAAGATCGG 420  
GTGCCCCACT CTCGGAATTC CATCACCTC ACCAACCTCA CTCCAGGCAC AGAGTATGTG 480  
GTCAGCATCG TTGCTCTTAA TGGCAGAGAG GAAAGTCCCT TATTGATTGG CCAACAATCA 540  
5 ACAGTTTCTG ATGTTCCGAG GGACCTGGAA GTTGTGCTG CGACCCCCAC CAGCCTACTG 600  
ATCAGCTGGG ATGCTCCTGC TGTCACAGTG AGATATTACA GGATCACTTA CGGAGAAACA 660  
GGAGGAAATA GCCCTGTCCA GGAGTTCCTG GTGCCTGGGA GCAAGTCTAC AGCTACCATC 720  
AGCGGCCTTA AACCTGGAGT TGATTATACC ATCACTGTGT ATGCTGTCAC TGGCCGTGGA 780  
GACAGCCCCG CAAGCAGCAA GCCAATTTCC ATTAATTACC GAACAGAAAT TGACAAACCA 840  
10 TCCACTAGCG CTATTCCTGC ACCAACTGAC CTGAAGTTCA CTCAGGTCAC ACCCACAAGC 900  
CTGAGCGCCC AGTGGACACC ACCCAATGTT CAGCTCACTG GATATCGAGT GCGGGTGACC 960  
CCCAAGGAGA AGACCGGACC AATGAAAGAA ATCAACCTTG CTCCTGACAG CTCATCCGTG 1020  
GTTGTATCAG GACTTATGGT GGCCACCAAA TATGAAGTGA GTGTCTATGC TCTTAAGGAC 1080  
ACTTTGACAA GCAGACCAGC TCAGGGTGTT GTCACCACTC TGGAGAATGT CAGCCCACCA 1140  
15 AGAAGGGCTC GTGTGACAGA TGCTACTGAG ACCACCATCA CCATTAGCTG GAGAACCAAG 1200  
ACTGAGACGA TCACTGGCTT CCAAGTTGAT GCCGTTCCAG CCAATGGCCA GACTCCAATC 1260  
CAGAGAACCA TCAAGCCAGA TGTCAGAAGC TACACCATCA CAGGTTTACA ACCAGGCACT 1320  
GACTACAAGA TCTACCTGTA CACCTTGAAT GACAATGCTC GGAGCTCCCC TGTGGTCATC 1380  
GACGCCTCCA CTGCCATTGA TGCACCATCC AACCTGCGTT TCCTGGCCAC CACACCCAAT 1440  
20 TCCTTGCTGG TATCATGGCA GCCGCCACGT GCCAGGATTA CCGGCTACAT CATCAAGTAT 1500  
GAGAAGCCTG GGTCTCCTCC CAGAGAAGTG GTCCCTCGGC CCCGCCCTGG TGTCACAGAG 1560  
GCTACTATTA CTGGCCTGGA ACCGGGAACC GAATATACAA TTTATGTCAT TGCCCTGAAG 1620  
AATAATCAGA AGAGCGAGCC CCTGATTGGA AGGAAAAAGA CTAGCGCTAT TCCTGCACCA 1680  
ACTGACCTGA AGTTCACTCA GGTCACACCC ACAAGCCTGA GCGCCCAGTG GACACCACCC 1740  
25 AATGTTTCAGC TCACTGGATA TCGAGTGCGG GTGACCCCCA AGGAGAAGAC CGGACCAATG 1800

AAAGAAATCA ACCTTGCTCC TGACAGCTCA TCCGTGGTTG TATCAGGACT TATGGTGGCC 1960  
ACCAAATATG AAGTGAGTGT CTATGCTCTT AAGGACACTT TGACAAGCAG ACCAGCTCAG 1920  
GGTGTGTGCA CCACTCTGGA GAATGTCAGC CCACCAAGAA GGGCTCGTGT GACAGATGCT 1980  
ACTGAGACCA CCATCACCAT TAGCTGGAGA ACCAAGACTG AGACGATCAC TGGCTTCCAA 2040  
5 GTTGATGCCG TTCCAGCCAA TGGCCAGACT CCAATCCAGA GAACCATCAA GCCAGATGTC 2100  
AGAAGCTACA CCATCACAGG TTTACAACCA GGCCTGACT ACAAGATCTA CCTGTACACC 2160  
TTGAATGACA ATGCTCGGAG CTCCCCTGTG GTCATCGACG CCTCCACTGC CATTGATGCA 2220  
CCATCCAACC TGCCTTTCCT GGCCACCACA CCCAATTCCT TGCTGGTATC ATGGCAGCCG 2280  
CCACGTGCCA GGATTACCGG CTACATCATC AAGTATGAGA AGCCTGGGTC TCCTCCCAGA 2340  
GAAGTGGTCC CTCGGCCCCG CCCTGGTGTC ACAGAGGCTA CTATTACTGG CCTGGAACCG 2400  
GGAACCGAAT ATACAATTTA TGTCATTGCC CTGAAGAATA ATCAGAAGAG CGAGCCCCTG 2460  
ATTGGAAGGA AAAAGACTAG T 2481

SEQ. ID No. 21

LENGTH: 472

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

20 Pro Thr Asp Leu Arg Phe Thr Asn Ile Gly Pro Asp Thr Met Arg  
1 5 10 15  
Val Thr Trp Ala Pro Pro Pro Ser Ile Asp Leu Thr Asn Phe Leu  
20 25 30  
Val Arg Tyr Ser Pro Val Lys Asn Glu Glu Asp Val Ala Glu Leu

35 40 45  
 Ser Ile Ser Pro Ser Asp Asn Ala Val Val Leu Thr Asn Leu Leu  
 50 55 60  
 Pro Gly Thr Glu Tyr Val Val Ser Val Ser Ser Val Tyr Glu Gln  
 5 65 70 75  
 His Glu Ser Thr Pro Leu Arg Gly Arg Gln Lys Thr Gly Leu Asp  
 80 85 90  
 Ser Pro Thr Gly Ile Asp Phe Ser Asp Ile Thr Ala Asn Ser Phe  
 95 100 105  
 Thr Val His Trp Ile Ala Pro Arg Ala Thr Ile Thr Gly Tyr Arg  
 110 115 120  
 Ile Arg His His Pro Glu His Phe Ser Gly Arg Pro Arg Glu Asp  
 125 130 135  
 Arg Val Pro His Ser Arg Asn Ser Ile Thr Leu Thr Asn Leu Thr  
 140 145 150  
 Pro Gly Thr Glu Tyr Val Val Ser Ile Val Ala Leu Asn Gly Arg  
 155 160 165  
 Glu Glu Ser Pro Leu Leu Ile Gly Gln Gln Ser Thr Val Ser Asp  
 170 175 180  
 20 Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu  
 185 190 195  
 Leu Ile Ser Trp Asp Ala Pro Ala Val Thr Val Arg Tyr Tyr Arg  
 200 205 210  
 Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe  
 25 215 220 225



	Thr	Val	Pro	Gly	Ser	Lys	Ser	Thr	Ala	Thr	Ile	Ser	Gly	Leu	Lys	
						230						235				240
	Pro	Gly	Val	Asp	Tyr	Thr	Ile	Thr	Val	Tyr	Ala	Val	Thr	Gly	Arg	
						245						250				255
5	Gly	Asp	Ser	Pro	Ala	Ser	Ser	Lys	Pro	Ile	Ser	Ile	Asn	Tyr	Arg	
						260						265				270
	Thr	Glu	Ile	Asp	Lys	Pro	Ser	Met	Ala	Ile	Pro	Ala	Pro	Thr	Asp	
						275						280				285
	Leu	Lys	Phe	Thr	Gln	Val	Thr	Pro	Thr	Ser	Leu	Ser	Ala	Gln	Trp	
10						290						295				300
	Thr	Pro	Pro	Asn	Val	Gln	Leu	Thr	Gly	Tyr	Arg	Val	Arg	Val	Thr	
						305						310				315
	Pro	Lys	Glu	Lys	Thr	Gly	Pro	Met	Lys	Glu	Ile	Asn	Leu	Ala	Pro	
						320						325				330
15	Asp	Ser	Ser	Ser	Val	Val	Val	Ser	Gly	Leu	Met	Val	Ala	Thr	Lys	
						335						340				345
	Tyr	Glu	Val	Ser	Val	Tyr	Ala	Leu	Lys	Asp	Thr	Leu	Thr	Ser	Arg	
						350						355				360
	Pro	Ala	Gln	Gly	Val	Val	Thr	Thr	Leu	Glu	Asn	Val	Ser	Pro	Pro	
20						365						370				375
	Arg	Arg	Ala	Arg	Val	Thr	Asp	Ala	Thr	Glu	Thr	Thr	Ile	Thr	Ile	
						380						385				390
	Ser	Trp	Arg	Thr	Lys	Thr	Glu	Thr	Ile	Thr	Gly	Phe	Gln	Val	Asp	
						395						400				405
25	Ala	Val	Pro	Ala	Asn	Gly	Gln	Thr	Pro	Ile	Gln	Arg	Thr	Ile	Lys	

410 415 420  
Pro Asp Val Arg Ser Tyr Thr Ile Thr Gly Leu Gln Pro Gly Thr  
425 430 435  
Asp Tyr Lys Ile Tyr Leu Tyr Thr Leu Asn Asp Asn Ala Arg Ser  
5 440 445 450  
Ser Pro Val Val Ile Asp Ala Ser Thr Ala Ile Asp Ala Pro Ser  
455 460 465  
Asn Leu Arg Phe Leu Ala Thr  
470

SEQ. ID No. 22

LENGTH: 457

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

Pro Thr Asp Leu Arg Phe Thr Asn Ile Gly Pro Asp Thr Met Arg  
1 5 10 15  
Val Thr Trp Ala Pro Pro Pro Ser Ile Asp Leu Thr Asn Phe Leu  
20 20 25 30  
Val Arg Tyr Ser Pro Val Lys Asn Glu Glu Asp Val Ala Glu Leu  
35 40 45  
Ser Ile Ser Pro Ser Asp Asn Ala Val Val Leu Thr Asn Leu Leu  
50 55 60

	Pro	Gly	Thr	Glu	Tyr	Val	Val	Ser	Val	Ser	Ser	Val	Tyr	Glu	Gln
						65				70					75
	His	Glu	Ser	Thr	Pro	Leu	Arg	Gly	Arg	Gln	Lys	Thr	Gly	Leu	Asp
						80				85					90
5	Ser	Pro	Thr	Gly	Ile	Asp	Phe	Ser	Asp	Ile	Thr	Ala	Asn	Ser	Phe
						95				100					105
	Thr	Val	His	Trp	Ile	Ala	Pro	Arg	Ala	Thr	Ile	Thr	Gly	Tyr	Arg
						110				115					120
	Ile	Arg	His	His	Pro	Glu	His	Phe	Ser	Gly	Arg	Pro	Arg	Glu	Asp
						125				130					135
	Arg	Val	Pro	His	Ser	Arg	Asn	Ser	Ile	Thr	Leu	Thr	Asn	Leu	Thr
						140				145					150
	Pro	Gly	Thr	Glu	Tyr	Val	Val	Ser	Ile	Val	Ala	Leu	Asn	Gly	Arg
						155				160					165
15	Glu	Glu	Ser	Pro	Leu	Leu	Ile	Gly	Gln	Gln	Ser	Thr	Val	Ser	Asp
						170				175					180
	Val	Pro	Arg	Asp	Leu	Glu	Val	Val	Ala	Ala	Thr	Pro	Thr	Ser	Leu
						185				190					195
	Leu	Ile	Ser	Trp	Asp	Ala	Pro	Ala	Val	Thr	Val	Arg	Tyr	Tyr	Arg
						200				205					210
20	Ile	Thr	Tyr	Gly	Glu	Thr	Gly	Gly	Asn	Ser	Pro	Val	Gln	Glu	Phe
						215				220					225
	Thr	Val	Pro	Gly	Ser	Lys	Ser	Thr	Ala	Thr	Ile	Ser	Gly	Leu	Lys
						230				235					240
25	Pro	Gly	Val	Asp	Tyr	Thr	Ile	Thr	Val	Tyr	Ala	Val	Thr	Gly	Arg

	245	250	255
Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile Ser Ile Asn Tyr Arg			
	260	265	270
Thr Glu Ile Asp Lys Pro Ser Met Asn Val Ser Pro Pro Arg Arg			
5	275	280	285
Ala Arg Val Thr Asp Ala Thr Glu Thr Thr Ile Thr Ile Ser Trp			
	290	295	300
Arg Thr Lys Thr Glu Thr Ile Thr Gly Phe Gln Val Asp Ala Val			
	305	310	315
Pro Ala Asn Gly Gln Thr Pro Ile Gln Arg Thr Ile Lys Pro Asp			
	320	325	330
Val Arg Ser Tyr Thr Ile Thr Gly Leu Gln Pro Gly Thr Asp Tyr			
	335	340	345
Lys Ile Tyr Leu Tyr Thr Leu Asn Asp Asn Ala Arg Ser Ser Pro			
15	350	355	360
Val Val Ile Asp Ala Ser Thr Ala Ile Asp Ala Pro Ser Asn Leu			
	365	370	375
Arg Phe Leu Ala Thr Thr Pro Asn Ser Leu Leu Val Ser Trp Gln			
	380	385	390
20	395	400	405
Pro Pro Arg Ala Arg Ile Thr Gly Tyr Ile Ile Lys Tyr Glu Lys			
	410	415	420
Pro Gly Ser Pro Pro Arg Glu Val Val Pro Arg Pro Arg Pro Gly			
	425	430	435
25			
Val Thr Glu Ala Thr Ile Thr Gly Leu Glu Pro Gly Thr Glu Tyr			

Thr Ile Tyr Val Ile Ala Leu Lys Asn Asn Gln Lys Ser Glu Pro  
440 445 450  
Leu Ile Gly Arg Lys Lys Thr  
455

5 SEQ. ID No. 23

LENGTH: 549

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

Pro Thr Asp Leu Arg Phe Thr Asn Ile Gly Pro Asp Thr Met Arg  
1 5 10 15

Val Thr Trp Ala Pro Pro Pro Ser Ile Asp Leu Thr Asn Phe Leu  
20 25 30

Val Arg Tyr Ser Pro Val Lys Asn Glu Glu Asp Val Ala Glu Leu  
35 40 45

Ser Ile Ser Pro Ser Asp Asn Ala Val Val Leu Thr Asn Leu Leu  
50 55 60

Pro Gly Thr Glu Tyr Val Val Ser Val Ser Ser Val Tyr Glu Gln  
65 70 75

His Glu Ser Thr Pro Leu Arg Gly Arg Gln Lys Thr Gly Leu Asp  
80 85 90

Ser Pro Thr Gly Ile Asp Phe Ser Asp Ile Thr Ala Asn Ser Phe

	95	100	105
	Thr Val His Trp Ile Ala Pro Arg Ala Thr Ile Thr Gly Tyr Arg		
	110	115	120
	Ile Arg His His Pro Glu His Phe Ser Gly Arg Pro Arg Glu Asp		
5	125	130	135
	Arg Val Pro His Ser Arg Asn Ser Ile Thr Leu Thr Asn Leu Thr		
	140	145	150
	Pro Gly Thr Glu Tyr Val Val Ser Ile Val Ala Leu Asn Gly Arg		
	155	160	165
10	Glu Glu Ser Pro Leu Leu Ile Gly Gln Gln Ser Thr Val Ser Asp		
	170	175	180
	Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu		
	185	190	195
	Leu Ile Ser Trp Asp Ala Pro Ala Val Thr Val Arg Tyr Tyr Arg		
15	200	205	210
	Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe		
	215	220	225
	Thr Val Pro Gly Ser Lys Ser Thr Ala Thr Ile Ser Gly Leu Lys		
	230	235	240
20	Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Gly Arg		
	245	250	255
	Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile Ser Ile Asn Tyr Arg		
	260	265	270
	Thr Glu Ile Asp Lys Pro Ser Met Ala Ile Pro Ala Pro Thr Asp		
25	275	280	285

62259  
10  
15  
20  
25

	Leu	Lys	Phe	Thr	Gln	Val	Thr	Pro	Thr	Ser	Leu	Ser	Ala	Gln	Trp
					290					295					300
	Thr	Pro	Pro	Asn	Val	Gln	Leu	Thr	Gly	Tyr	Arg	Val	Arg	Val	Thr
					305					310					315
5	Pro	Lys	Glu	Lys	Thr	Gly	Pro	Met	Lys	Glu	Ile	Asn	Leu	Ala	Pro
					320					325					330
	Asp	Ser	Ser	Ser	Val	Val	Val	Ser	Gly	Leu	Met	Val	Ala	Thr	Lys
					335					340					345
	Tyr	Glu	Val	Ser	Val	Tyr	Ala	Leu	Lys	Asp	Thr	Leu	Thr	Ser	Arg
					350					355					360
	Pro	Ala	Gln	Gly	Val	Val	Thr	Thr	Leu	Glu	Asn	Val	Ser	Pro	Pro
					365					370					375
	Arg	Arg	Ala	Arg	Val	Thr	Asp	Ala	Thr	Glu	Thr	Thr	Ile	Thr	Ile
					380					385					390
	Ser	Trp	Arg	Thr	Lys	Thr	Glu	Thr	Ile	Thr	Gly	Phe	Gln	Val	Asp
					395					400					405
	Ala	Val	Pro	Ala	Asn	Gly	Gln	Thr	Pro	Ile	Gln	Arg	Thr	Ile	Lys
					410					415					420
	Pro	Asp	Val	Arg	Ser	Tyr	Thr	Ile	Thr	Gly	Leu	Gln	Pro	Gly	Thr
					425					430					435
	Asp	Tyr	Lys	Ile	Tyr	Leu	Tyr	Thr	Leu	Asn	Asp	Asn	Ala	Arg	Ser
					440					445					450
	Ser	Pro	Val	Val	Ile	Asp	Ala	Ser	Thr	Ala	Ile	Asp	Ala	Pro	Ser
					455					460					465
25	Asn	Leu	Arg	Phe	Leu	Ala	Thr	Thr	Pro	Asn	Ser	Leu	Leu	Val	Ser





20

5

10

15

20

25

	230	235	240
Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Gly Arg			
	245	250	255
Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile Ser Ile Asn Tyr Arg			
	260	265	270
Thr Glu Ile Asp Lys Pro Ser Met Ala Ile Pro Ala Pro Thr Asp			
	275	280	285
Leu Lys Phe Thr Gln Val Thr Pro Thr Ser Leu Ser Ala Gln Trp			
	290	295	300
Thr Pro Pro Asn Val Gln Leu Thr Gly Tyr Arg Val Arg Val Thr			
	305	310	315
Pro Lys Glu Lys Thr Gly Pro Met Lys Glu Ile Asn Leu Ala Pro			
	320	325	330
Asp Ser Ser Ser Val Val Val Ser Gly Leu Met Val Ala Thr Lys			
	335	340	345
Tyr Glu Val Ser Val Tyr Ala Leu Lys Asp Thr Leu Thr Ser Arg			
	350	355	360
Pro Ala Gln Gly Val Val Thr Thr Leu Glu Asn Val Ser Pro Pro			
	365	370	375
Arg Arg Ala Arg Val Thr Asp Ala Thr Glu Thr Thr Ile Thr Ile			
	380	385	390
Ser Trp Arg Thr Lys Thr Glu Thr Ile Thr Gly Phe Gln Val Asp			
	395	400	405
Ala Val Pro Ala Asn Gly Gln Thr Pro Ile Gln Arg Thr Ile Lys			
	410	415	420

	Pro	Asp	Val	Arg	Ser	Tyr	Thr	Ile	Thr	Gly	Leu	Gln	Pro	Gly	Thr	
					425					430						435
	Asp	Tyr	Lys	Ile	Tyr	Leu	Tyr	Thr	Leu	Asn	Asp	Asn	Ala	Arg	Ser	
					440					445						450
5	Ser	Pro	Val	Val	Ile	Asp	Ala	Ser	Thr	Ala	Ile	Asp	Ala	Pro	Ser	
					455					460						465
	Asn	Leu	Arg	Phe	Leu	Ala	Thr	Thr	Pro	Asn	Ser	Leu	Leu	Val	Ser	
					470					475						480
	Trp	Gln	Pro	Pro	Arg	Ala	Arg	Ile	Thr	Gly	Tyr	Ile	Ile	Lys	Tyr	
					485					490						495
	Glu	Lys	Pro	Gly	Ser	Pro	Pro	Arg	Glu	Val	Val	Pro	Arg	Pro	Arg	
					500					505						510
	Pro	Gly	Val	Thr	Glu	Ala	Thr	Ile	Thr	Gly	Leu	Glu	Pro	Gly	Thr	
					515					520						525
15	Glu	Tyr	Thr	Ile	Tyr	Val	Ile	Ala	Leu	Lys	Asn	Asn	Gln	Lys	Ser	
					530					535						540
	Glu	Pro	Leu	Ile	Gly	Arg	Lys	Lys	Thr	Asp	Glu	Leu	Pro	Gln	Leu	
					545					550						555
	Val	Thr	Leu	Pro	His	Pro	Asn	Leu	His	Gly	Pro	Glu	Ile	Leu	Asp	
20					560					565						570
	Val	Pro	Ser	Thr												

SEQ. ID No. 25

LENGTH: 274

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

5 Pro Thr Asp Leu Arg Phe Thr Asn Ile Gly Pro Asp Thr Met Arg  
1 5 10 15  
Val Thr Trp Ala Pro Pro Pro Ser Ile Asp Leu Thr Asn Phe Leu  
20 25 30  
Val Arg Tyr Ser Pro Val Lys Asn Glu Glu Asp Val Ala Glu Leu  
35 40 45  
Ser Ile Ser Pro Ser Asp Asn Ala Val Val Leu Thr Asn Leu Leu  
50 55 60  
Pro Gly Thr Glu Tyr Val Val Ser Val Ser Ser Val Tyr Glu Gln  
65 70 75  
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SEQ. ID No. 26

LENGTH: 1374

TYPE: nucleic acid

20 STRANDEDNESS: double

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (DNA encoding an artificial polypeptide)

SEQUENCE:

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GTTGCTCTTA ATGGCAGAGA GGAAAGTCCC TTATTGATTG GCCAACAATC AACAGTTTCT 540  
10 GATGTTCCGA GGGACCTGGA AGTTGTTGCT GCGACCCCCA CCAGCCTACT GATCAGCTGG 600  
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GCAAGCAGCA AGCCAATTTT CATTAATTAC CGAACAGAAA TTGACAAACC ATCCATGGCA 840  
15 GCCGGGAGCA TCACCACGCT GCCCGCCTTG CCCGAGGATG GCGGCAGCGG CGCCTTCCCG 900  
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CAACTTCAAG CAGAAGAGAG AGGAGTTGTG TCTATCAAAG GAGTGTGTGC TAACCGTTAC 1080  
CTGGCTATGA AGGAAGATGG AAGATTACTG GCTTCTAAAT GTGTTACGGA TGAGTGT TTC 1140  
20 TTTTTTGAAC GATTGGAATC TAATAACTAC AATACTTACC GCTCAAGGAA ATACACCAGT 1200  
TGGTATGTGG CACTGAAACG AACTGGGCAG TATAAACTTG GATCCAAAAC AGGACCTGGG 1260  
CAGAAAGCTA TACTTTTTCT TCCAATGTCT GCTGCTAGCG ACGAGCTTCC CCAACTGGTA 1320  
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LENGTH: 1416

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

5 MOLECULAR TYPE: other nucleic acid (DNA encoding an artificial polypeptide)

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CCAGCTCAGG GTGTTGTCAC CACTCTGGAG AATGTCAGCC CACCAAGAAG GGCTCGTGTG 1140  
ACAGATGCTA CTGAGACCAC CATCACCATT AGCTGGAGAA CCAAGACTGA GACGATCACT 1200  
GGCTTCCAAG TTGATGCCGT TCCAGCCAAT GGCCAGACTC CAATCCAGAG AACCATCAAG 1260  
CCAGATGTCA GAAGCTACAC CATCACAGGT TTACAACCAG GCACTGACTA CAAGATCTAC 1320  
5 CTGTACACCT TGAATGACAA TGCTCGGAGC TCCCCTGTGG TCATCGACGC CTCCACTGCC 1380  
ATTGATGCAC CATCCAACCT GCGTTTCCTG GCCACC 1416

SEQ. ID No. 28

LENGTH: 35

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

Gly Gly Arg Gly Thr Pro Gly Lys Pro Gly Pro Arg Gly Gln Arg  
15           1                   5                   10                   15  
Gly Pro Thr Gly Pro Arg Gly Glu Arg Gly Pro Arg Gly Ile Thr  
                 20                   25                   30  
Gly Lys Pro Gly Pro  
                 35

20 SEQ. ID No. 29

LENGTH: 302

TYPE: amino acid

STRANDEDNESS: single



MOLECULAR TYPE: peptide

Pro Thr Asp Leu Arg Phe Thr Asn Ile Gly Pro Asp Thr Met Arg

Val Thr Trp Ala Pro Pro Pro Ser Ile Asp Leu Thr Asn Phe Leu

20 25 30

Val Arg Tyr Ser Pro Val Lys Asn Glu Glu Asp Val Ala Glu Leu

35                      40                      45

Ser Ile Ser Pro Ser Asp Asn Ala Val Val Leu Thr Asn Leu Leu

50                      55                      60

Pro Gly Thr Glu Tyr Val Val Ser Val Ser Ser Val Tyr Glu Gln

65                      70                      75

His Glu Ser Thr Pro Leu Arg Gly Arg Gln Lys Thr Gly Leu Asp

80                      85                      90

Ser Pro Thr Gly Ile Asp Phe Ser Asp Ile Thr Ala Asn Ser Phe

95                      100                      105

Thr Val His Trp Ile Ala Pro Arg Ala Thr Ile Thr Gly Tyr Arg

110                      115                      120

Ile Arg His His Pro Glu His Phe Ser Gly Arg Pro Arg Glu Asp

125                      130                      135

Arg Val Pro His Ser Arg Asn Ser Ile Thr Leu Thr Asn Leu Thr

140                      145                      150

Pro Gly Thr Glu Tyr Val Val Ser Ile Val Ala Leu Asn Gly Arg

155                      160                      165

Glu	Glu	Ser	Pro	Leu	Leu	Ile	Gly	Gln	Gln	Ser	Thr	Val	Ser	Asp	
				170				175						180	
Val	Pro	Arg	Asp	Leu	Glu	Val	Val	Ala	Ala	Thr	Pro	Thr	Ser	Leu	
				185				190						195	
5	Leu	Ile	Ser	Trp	Asp	Ala	Pro	Ala	Val	Thr	Val	Arg	Tyr	Tyr	Arg
				200				205						210	
	Ile	Thr	Tyr	Gly	Glu	Thr	Gly	Gly	Asn	Ser	Pro	Val	Gln	Glu	Phe
				215				220						225	
	Thr	Val	Pro	Gly	Ser	Lys	Ser	Thr	Ala	Thr	Ile	Ser	Gly	Leu	Lys
				230				235						240	
	Pro	Gly	Val	Asp	Tyr	Thr	Ile	Thr	Val	Tyr	Ala	Val	Thr	Gly	Arg
				245				250						255	
	Gly	Asp	Ser	Pro	Ala	Ser	Ser	Lys	Pro	Ile	Ser	Ile	Asn	Tyr	Arg
				260				265						270	
15	Thr	Glu	Ile	Asp	Lys	Pro	Ser	Asp	Glu	Leu	Pro	Gln	Leu	Val	Thr
				275				280						285	
	Leu	Pro	His	Pro	Asn	Leu	His	Gly	Pro	Glu	Ile	Leu	Asp	Val	Pro
				290				295						300	

Ser Thr

20 SEQ. ID No. 30  
 LENGTH: 573  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

	Met	Ala	Ala	Ser	Ala	Ile	Pro	Ala	Pro	Thr	Asp	Leu	Lys	Phe	Thr	
						5					10					15
5	Gln	Val	Thr	Pro	Thr	Ser	Leu	Ser	Ala	Gln	Trp	Thr	Pro	Pro	Asn	
						20					25					30
	Val	Gln	Leu	Thr	Gly	Tyr	Arg	Val	Arg	Val	Thr	Pro	Lys	Glu	Lys	
						35					40					45
	Thr	Gly	Pro	Met	Lys	Glu	Ile	Asn	Leu	Ala	Pro	Asp	Ser	Ser	Ser	
						50					55					60
	Val	Val	Val	Ser	Gly	Leu	Met	Val	Ala	Thr	Lys	Tyr	Glu	Val	Ser	
						65					70					75
	Val	Tyr	Ala	Leu	Lys	Asp	Thr	Leu	Thr	Ser	Arg	Pro	Ala	Gln	Gly	
						80					85					90
	Val	Val	Thr	Thr	Leu	Glu	Asn	Val	Ser	Pro	Pro	Arg	Arg	Ala	Arg	
						95					100					105
	Val	Thr	Asp	Ala	Thr	Glu	Thr	Thr	Ile	Thr	Ile	Ser	Trp	Arg	Thr	
						110					115					120
	Lys	Thr	Glu	Thr	Ile	Thr	Gly	Phe	Gln	Val	Asp	Ala	Val	Pro	Ala	
						125					130					135
20	Asn	Gly	Gln	Thr	Pro	Ile	Gln	Arg	Thr	Ile	Lys	Pro	Asp	Val	Arg	
						140					145					150
	Ser	Tyr	Thr	Ile	Thr	Gly	Leu	Gln	Pro	Gly	Thr	Asp	Tyr	Lys	Ile	
						155					160					165
25	Tyr	Leu	Tyr	Thr	Leu	Asn	Asp	Asn	Ala	Arg	Ser	Ser	Pro	Val	Val	

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	170	175	180
Ile Asp Ala Ser Thr Ala Ile Asp Ala Pro Ser Asn Leu Arg Phe			
	185	190	195
Leu Ala Thr Thr Pro Asn Ser Leu Leu Val Ser Trp Gln Pro Pro			
	200	205	210
Arg Ala Arg Ile Thr Gly Tyr Ile Ile Lys Tyr Glu Lys Pro Gly			
	215	220	225
Ser Pro Pro Arg Glu Val Val Pro Arg Pro Arg Pro Gly Val Thr			
	230	235	240
Glu Ala Thr Ile Thr Gly Leu Glu Pro Gly Thr Glu Tyr Thr Ile			
	245	250	255
Tyr Val Ile Ala Leu Lys Asn Asn Gln Lys Ser Glu Pro Leu Ile			
	260	265	270
Gly Arg Lys Lys Thr Ala Ile Pro Ala Pro Thr Asp Leu Lys Phe			
	275	280	285
Thr Gln Val Thr Pro Thr Ser Leu Ser Ala Gln Trp Thr Pro Pro			
	290	295	300
Asn Val Gln Leu Thr Gly Tyr Arg Val Arg Val Thr Pro Lys Glu			
	305	310	315
Lys Thr Gly Pro Met Lys Glu Ile Asn Leu Ala Pro Asp Ser Ser			
	320	325	330
Ser Val Val Val Ser Gly Leu Met Val Ala Thr Lys Tyr Glu Val			
	335	340	345
Ser Val Tyr Ala Leu Lys Asp Thr Leu Thr Ser Arg Pro Ala Gln			
	350	355	360

365 370 375  
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Gly	Val	Val	Thr	Thr	Leu	Glu	Asn	Val	Ser	Pro	Pro	Arg	Arg	Ala
					365				370					375
Arg	Val	Thr	Asp	Ala	Thr	Glu	Thr	Thr	Ile	Thr	Ile	Ser	Trp	Arg
					380				385					390
Thr	Lys	Thr	Glu	Thr	Ile	Thr	Gly	Phe	Gln	Val	Asp	Ala	Val	Pro
					395				400					405
Ala	Asn	Gly	Gln	Thr	Pro	Ile	Gln	Arg	Thr	Ile	Lys	Pro	Asp	Val
					410				415					420
Arg	Ser	Tyr	Thr	Ile	Thr	Gly	Leu	Gln	Pro	Gly	Thr	Asp	Tyr	Lys
					425				430					435
Ile	Tyr	Leu	Tyr	Thr	Leu	Asn	Asp	Asn	Ala	Arg	Ser	Ser	Pro	Val
					440				445					450
Val	Ile	Asp	Ala	Ser	Thr	Ala	Ile	Asp	Ala	Pro	Ser	Asn	Leu	Arg
					455				460					465
Phe	Leu	Ala	Thr	Thr	Pro	Asn	Ser	Leu	Leu	Val	Ser	Trp	Gln	Pro
					470				475					480
Pro	Arg	Ala	Arg	Ile	Thr	Gly	Tyr	Ile	Ile	Lys	Tyr	Glu	Lys	Pro
					485				490					495
Gly	Ser	Pro	Pro	Arg	Glu	Val	Val	Pro	Arg	Pro	Arg	Pro	Gly	Val
					500				505					510
Thr	Glu	Ala	Thr	Ile	Thr	Gly	Leu	Glu	Pro	Gly	Thr	Glu	Tyr	Thr
					515				520					525
Ile	Tyr	Val	Ile	Ala	Leu	Lys	Asn	Asn	Gln	Lys	Ser	Glu	Pro	Leu
					530				535					540
Ile	Gly	Arg	Lys	Lys	Thr	Ser	Asp	Glu	Leu	Pro	Gln	Leu	Val	Thr

545 550 555  
Leu Pro His Pro Asn Leu His Gly Pro Glu Ile Leu Asp Val Pro  
560 565 570  
Ser Thr Ser

5 SEQ. ID No. 31  
LENGTH: 37  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
10 MOLECULAR TYPE: other nucleic acid (synthetic DNA)  
SEQUENCE:  
AAACCATGGC AGCTAGCAAT GTCAGCCCAC CAAGAAG 37

15 SEQ. ID No. 32  
LENGTH: 37  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULAR TYPE: other nucleic acid (synthetic DNA)  
SEQUENCE:  
20 AAAGGATCCC TAACTAGTGG AAGGAACATC CAAGATC 37

SEQ. ID No. 33  
LENGTH: 1722

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (DNA encoding an artificial polypeptide)

SEQUENCE:

ATGGCAGCTA GCGCTATTCC TGCACCAACT GACCTGAAGT TCACTCAGGT CACACCCACA 60  
AGCCTGAGCG CCCAGTGGAC ACCACCCAAT GTTCAGCTCA CTGGATATCG AGTGCGGGTG 120  
ACCCCAAGG AGAAGACCGG ACCAATGAAA GAAATCAACC TTGCTCCTGA CAGCTCATCC 180  
GTGGTTGTAT CAGGACTTAT GGTGGCCACC AAATATGAAG TGAGTGTCTA TGCTCTTAAG 240  
GACACTTTGA CAAGCAGACC AGCTCAGGGT GTTGTACCA CTCTGGAGAA TGTCAGCCCA 300  
CCAAGAAGGG CTCGTGTGAC AGATGCTACT GAGACCACCA TCACCATTAG CTGGAGAACC 360  
AAGACTGAGA CGATCACTGG CTTCCAAGTT GATGCCGTTT CAGCCAATGG CCAGACTCCA 420  
ATCCAGAGAA CCATCAAGCC AGATGTCAGA AGCTACACCA TCACAGGTTT ACAACCAGGC 480  
ACTGACTACA AGATCTACCT GTACACCTTG AATGACAATG CTCGGAGCTC CCCTGTGGTC 540  
ATCGACGCCT CCACTGCCAT TGATGCACCA TCCAACCTGC GTTTCCTGGC CACCACACCC 600  
AATTCCTTGC TGGTATCATG GCAGCCGCCA CGTGCCAGGA TTACCGGCTA CATCATCAAG 660  
TATGAGAAGC CTGGGTCTCC TCCAGAGAA GTGGTCCCTC GGCCCCGCCC TGGTGTCA 720  
GAGGCTACTA TTA CTGGCCT GGAACCGGGA ACCGAATATA CAATTTATGT CATTGCCCTG 780  
AAGAATAATC AGAAGAGCGA GCCCCTGATT GGAAGGAAAA AGACTAGCGC TATTCCTGCA 840  
CCA ACTGACC TGAAGTTCAC TCAGGTCACA CCCACAAGCC TGAGCGCCCA GTGGACACCA 900  
CCAATGTTC AGCTCACTGG ATATCGAGTG CGGGTGACCC CCAAGGAGAA GACCGGACCA 960  
ATGAAAGAAA TCAACCTTGC TCCTGACAGC TCATCCGTGG TTGTATCAGG ACTTATGGTG 1020  
GCCACCAAAT ATGAAGTGAG TGTCTATGCT CTTAAGGACA CTTTGACAAG CAGACCAGCT 1080  
CAGGGTGTTC TCACCACTCT GGAGAATGTC AGCCCACCAA GAAGGGCTCG TGTGACAGAT 1140

GCTACTGAGA CCACCATCAC CATTAGCTGG AGAACCAAGA CTGAGACGAT CACTGGCTTC 1200  
CAAGTTGATG CCGTTCCAGC CAATGGCCAG ACTCCAATCC AGAGAACCAT CAAGCCAGAT 1260  
GTCAGAAGCT ACACCATCAC AGGTTTACAA CCAGGCACTG ACTACAAGAT CTACCTGTAC 1320  
ACCTTGAATG ACAATGCTCG GAGCTCCCCT GTGGTCATCG ACGCCTCCAC TGCCATTGAT 1380  
5 GCACCATCCA ACCTGCGTTT CCTGGCCACC ACACCCAATT CCTTGCTGGT ATCATGGCAG 1440  
CCGCCACGTG CCAGGATTAC CGGCTACATC ATCAAGTATG AGAAGCCTGG GTCTCCTCCC 1500  
AGAGAAGTGG TCCCTCGGCC CCGCCCTGGT GTCACAGAGG CTACTATTAC TGGCCTGGAA 1560  
CCGGAACCG AATATACAAT TTATGTCATT GCCCTGAAGA ATAATCAGAA GAGCGAGCCC 1620  
CTGATTGGAA GGAAAAAGAC TAGCGACGAG CTTCCCCAAC TGGTAACCCT TCCACACCCC 1680  
AATCTTCATG GACCAGAGAT CTTGGATGTT CCTTCCACTA GT 1722

SEQ. ID No. 34

LENGTH: 412

TYPE: amino acid

STRANDEDNESS: single

15 TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln

5 10 15

20 Pro Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu

20 25 30

His Leu Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys

35 40 45

Phe Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp



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SEQ. ID No. 35

LENGTH: 24

TYPE: nucleic acid

STRANDEDNESS: single

5 TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

GCTCCCTCTG GGCCTCCCAG TCCT

24

SEQ. ID No. 36

LENGTH: 24

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (synthetic DNA)

15 SEQUENCE:

GTTGGTGAGG GAGGTGGTGG ATAT

24

SEQ. ID No. 37

LENGTH: 33

TYPE: nucleic acid

20 STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

GGCCTCCCGA ATTCCGGTGC CCCACCACGC CTC

33

SEQ. ID No. 38

LENGTH: 33

TYPE: nucleic acid

5 STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

CCCACGTGGA TCCATGGCTA ATCTGTCCCC TGT

33

SEQ. ID No. 39

LENGTH: 1239

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

15 MOLECULAR TYPE: other nucleic acid (DNA encoding an artificial polypeptide)

SEQUENCE:

ATGTCCCCTA TACTAGGTTA TTGGAAAATT AAGGGCCTTG TGCAACCCAC TCGACTTCTT 60

TTGGAATATC TTGAAGAAAA ATATGAAGAG CATTTGTATG AGCGCGATGA AGGTGATAAA 120

20 TGGCGAAACA AAAAGTTTGA ATTGGGTTTG GAGTTTCCCA ATCTTCCTTA TTATATTGAT 180

GGTGATGTTA AATTAACACA GTCTATGGCC ATCATACGTT ATATAGCTGA CAAGCACAAC 240

ATGTTGGGTG GTTGTCCAAA AGAGCGTGCA GAGATTTCAA TGCTTGAAGG AGCGGTTTGT 300

GATATTAGAT ACGGTGTTTC GAGAATTGCA TATAGTAAAG ACTTTGAAAC TCTCAAAGTT 360

GATTTTCTTA GCAAGCTACC TGAAATGCTG AAAATGTTTCG AAGATCGTTT ATGTCATAAA 420  
ACATATTTAA ATGGTGATCA TGTAACCCAT CCTGACTTCA TGTTGTATGA CGCTCTTGAT 480  
GTTGTTTTAT ACATGGACCC AATGTGCCTG GATGCGTTCC CAAAATTAGT TTGTTTTAAA 540  
AAACGTATTG AAGCTATCCC ACAAATTGAT AAGTACTTGA AATCCAGCAA GTATATAGCA 600  
5 TGGCCTTTGC AGGGCTGGCA AGCCACGTTT GGTGGTGGCG ACCATCCTCC AAAATCGGAT 660  
CTGATCGAAG GTCGTGGGAT CCCCAGGAAT TCCGGTGCCC CACCACGCCT CATCTGTGAC 720  
AGCCGAGTCC TGCAGAGGTA CCTCTTGGAG GCCAAGGAGG CCGAGAATAT CACGACGGGC 780  
TGTGCTGAAC ACTGCAGCTT GAATGAGAAT ATCACTGTCC CAGACACCAA AGTTAATTTTC 840  
TATGCCTGGA AGAGGATGGA GGTCGGGCAG CAGGCCGTAG AAGTCTGGCA GGGCCTGGCC 900  
10 CTGCTGTCGG AAGCTGTCCT GCGGGGCCAG GCCCTGTTGG TCAACTCTTC CCAGCCGTGG 960  
GAGCCCCTGC AGCTGCATGT GGATAAAGCC GTCAGTGGCC TTCGCAGCCT CACCACTCTG 1020  
CTTCGGGCTC TGGGAGCCCA GAAGGAAGCC ATCTCCCCTC CAGATGCGGC CTCAGCTGCT 1080  
CCACTCCGAA CAATCACTGC TGACACTTTC CGAAACTCT TCCGAGTCTA CTCCAATTTTC 1140  
CTCCGGGGAA AGCTGAAGCT GTACACAGGG GAGGCCTGCA GGACAGGGGA CAGATTAGCC 1200  
15 ATGGATCCTC TAGAGTCGAC TCGAGCGGCC GCATCGTGA 1239